Applicant: Andrzej S. Krolewski, et al. Attorney's Docket No.: 10276-078001 / JDP-078

Serial No.: 10/694,685

Filed : October 28, 2003

Page : 2 of 5

Amendments to the Specification:

Insert the paper copy of the Sequence Listing filed herewith following the Oath/Declaration.

Please replace the paragraph beginning at page 23, line 11 with the following amended paragraph:

FIG.6A-C is a GCG gap alignment of predicted Diff40 long form (BAA20840) (SEQ ID NO:[23]37, top sequence) with the predicted Diff40-short form NCBI Ref Seq protein sequence (NP_56948) (SEQ ID NO:[24]38, bottom sequence). A default gap penalty of -8/-2 was used in the alignment.

Please replace the paragraph beginning at page 23, line 15 with the following amended paragraph:

FIG. 7A-C is a GCG bestfit alignment of predicted Diff40 long form (BAA20840) (SEQ ID NO:[23]39) with the predicted T2DM-1a amino acid sequence (SEQ ID NO:2). A default gap penalty of -8/-2 was used. The amino and carboxyl termini of the Diff40 long form show similarity to T2DM-1a. (Underlined sequence = present in diff40 long form only. Double underlined residues = end of Diff40-short form and end of long/short T2DM-1 common sequence.)

Please replace the paragraph beginning at page 23, line 21 with the following amended paragraph:

FIG.8A-B is a GCG bestfit alignment of predicted Diff40 short form (BAA20840) (SEQ ID NO:40) with the predicted T2DM-1b (short form) (SEQ ID NO:4). A default gap penalty of -8/-2 was used.

Applicant: Andrzej S. Krolewski, et al. Attorney's Docket No.: 10276-078001 / JDP-078

Serial No.: 10/694,685

Filed : October 28, 2003

Page : 3 of 5

Please replace the paragraph beginning at page 26, line 1 with the following amended paragraph:

Figure 6 shows an alignment of Diff40-Long form (SEQ ID NO:[23]37) with T2DM-1a (SEQ ID NO:2). Figure 7 shows the alignment of Diff40-short form (SEQ ID NO:[24]39) with T2DM-1b. The amino and carboxyl termini of the Diff40 Long form show very significant similarity to T2DM-1a and probably present conserved domains. The central region of the proteins, i.e., Diff40: amino acid residues 355 to 726 of SEQ ID NO:2, T2DM-1: 356-602 is least well conserved, and contains pronounced [S,P,E] compositional biases. The short isoforms of these homologs terminate in the middle of this central region.

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Serial No.: 10/694,685

Filed: October 28, 2003

Page : 4 of 5

Amendments to the Drawings:

The attached replacement sheets of drawings includes amendments to Fig. 6C, Fig. 7C and Fig. 8B. The amendments merely update the sequence identifier numbers (SEQ ID NOs).

Attachments following last page of this Amendment:

Replacement Sheets (3 pages)
Annotated Sheets Showing Changes (3 pages)